

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:13:46 ; Search time 17 seconds

(without alignments)  
672.941 Million cell updates/sec

Title: US-10-015-967-2

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMTSMV.....SRACQFLKOCQLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.5	12.0	477	2	hypothetical prote
2	77	12.0	2269	1	genome polypeptide
3	74.5	11.6	448	2	vitamin D receptor
4	73.5	11.4	70	2	vitamin D receptor
5	71.5	11.1	108	2	steroid receptor p
6	71	11.0	411	2	steroid receptor p
7	71	11.0	2262	2	steroid receptor p
8	71	11.0	3190	2	steroid receptor p
9	70.5	10.9	1283	2	steroid receptor p
10	70	10.9	543	2	steroid receptor p
11	70	10.9	746	2	steroid receptor p
12	70	10.9	1095	2	steroid receptor p
13	70	10.9	1620	2	steroid receptor p
14	69.5	10.8	221	2	steroid receptor p
15	69.5	10.8	575	1	steroid receptor p
16	69	10.7	200	2	steroid receptor p
17	68.5	10.6	381	2	steroid receptor p
18	68.5	10.6	422	2	steroid receptor p
19	68.5	10.6	423	2	steroid receptor p
20	68.5	10.6	427	2	steroid receptor p
21	68.5	10.6	427	2	steroid receptor p
22	68.5	10.6	427	2	steroid receptor p
23	68.5	10.6	427	2	steroid receptor p
24	68	10.6	283	2	steroid receptor p
25	67	10.4	376	2	steroid receptor p
26	67	10.4	376	2	steroid receptor p
27	67	10.4	1062	2	steroid receptor p
28	67	10.4	1062	2	steroid receptor p
29	66.5	10.3	103	2	steroid receptor p

30	66.5	10.3	419	2	A57000	orphan receptor CO
31	66.5	10.3	422	2	I48305	gene CUP-1F1 prot
32	66.5	10.3	423	2	S02710	transcription fact
33	66	10.2	339	2	T36061	hypothetical prote
34	65.5	10.2	106	2	S60232	gibberellin-regula
35	65.5	10.2	397	2	S20617	transcription fact
36	65.5	10.2	413	2	H82270	hypothetical prote
37	65.5	10.2	425	2	JC7230	vitamin D receptor
38	65.5	10.2	646	2	S36586	El protein - human
39	65.5	10.2	706	2	JE0164	frizzled-6 protein
40	65	10.1	363	2	JC4748	polygalacturonase
41	65	10.1	440	2	JS0374	hypothetical 51.6k
42	65	10.1	1797	2	A55677	laminin beta-2 cha
43	64.5	10.0	359	2	B25960	Baldian ring 2 ch
44	64.5	10.0	622	2	I48733	protein kinase rok
45	64	9.9	227	2	I39313	zinc-finger protei

## ALIGNMENTS

## RESULT 1

T18801 hypothetical protein ZK131.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000

C:Accession: T18801; T27746

R:Pericy, C.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19024

A:Accession: T18801

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-477 <MT>

A:Cross-references: EMBL:293373; PIDN:CAB07552.1; GSPDB:GN00020; CESP:ZK131.11

A:Experimental source: clone C01B9

A:Reference number: Z20413

A:Accession: T27746

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-477 <MT>

A:Cross-references: EMBL:283245; PIDN:CAB05840.1; GSPDB:GN00020; CESP:ZK131.11

A:Experimental source: clone ZK131

A:Genetics: CESP:ZK131.11

A:Map position: 2

A:introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3; 432/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK131.11

Query Match 12.0%; Score 77.5; DB 2; Length 477;

Best Local Similarity 34.7%; Pred. No. 2.3;

Matches 25; Conservative 6; Mismatches 32; Indels 9; Gaps 3;

QY 46 GGOECCKDMFLRPRR---KMTVSGLPKQ--CPDHFKNVKKTRHQHRRKPKHS 100  
DB 290 GGNMNSNTTFLRATRFKKITTSATLPKKONSTMDNFQSSVFEEDTAHHNNMNG 349  
QY 101 RACQFLKOCQL 112  
DB 350 R---ILKRAPL 357

## RESULT 2

J01750 genome polypeptide - simian paramyxovirus SV41 (strain Toshiba/Chanock)

N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: simian paramyxovirus SV41

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 11-Jun-1999

C:Accession: J01750

R:Ogawa, M.; Mutsuga, N.; Tsurudome, M.; Kawano, M.; Matsumura, H.; Kusagawa, S.; Kom

J. Gen. Virol. 73, 2743-2750, 1992

A:Title: Nucleotide sequence analysis of the simian virus 41 gene encoding the large (L)

A:Reference number: JQ1750; MUID:93019033; PMID:1328485

A:Accession: JQ1750

A:Molecule type: mRNA

A:Residues: 1-2269 <OGA>

A:Cross-references: EMBL:X64275; NID:9433516; PIDD:CAA45569.1; PID:9433522

C:Genetics:

A:Gene: L

C:Superfamily: paramfluenza virus RNA-directed RNA polymerase

C:Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query Match 12.0%; Score 77; DB 1; Length 2269;

Best Local Similarity 27.5%; Pred. No. 10;

Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;

QY 13 PLMLMSVSSSLNPGVARGHNRGQAS-----RRMLQ-----EGSQEGB--CK 53

DB 422 PLSLPGNASKRS-----IELHNDNSEISYEYTLRHNKELSLIEFKKCFDDEPDESLIFMK 477

QY 54 DMFLAPRKREKMTYSGSLPRKQCPCDHFKGNVAKTRRORHN--EKPNKSR 101

DB 478 DKAISAPKEDMMSV-----FKRSLLKQRNRHRIIMPENFNR 514

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RESULT 3
150451
vitamin D receptor isoform A - Japanese quail
C:Species: Coturnix coturnix (Japanese quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C:Accession: 150451
R:Elaroussi, M.A.; Prah, J.M.; Deluca, H.F
Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
A:Title: The avian vitamin D receptors: primary structures and their origins.
A:Reference number: 150451, PMID:95062315; PMID:7972109
A:Accession: 150451
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-448 <E>A>
A:Cross-references: EMBL:U12641; NID:9595500; PIDD:AA56725.1; PID:9595501
C:Superfamily: unassigned erda-related proteins; erda transforming protein homology
C:Keywords: zinc finger
E:/42-362/Domain: erda transforming protein homology <ERBA>

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Query Match          11.6%; Score 74.5; DB 2; Length 448;
Best Local Similarity 32.9%; Pred.No.4.5;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

QY      50 CE-CRDMFLRAPRRKMTVSGLPKKQCPDHFNGVNRKTRHQRNHRKPKNHSACQFTLK 108
        |||::||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       61 CEECKKFFFRSMKRKMFT-----CP---FEGDCKITRDNR-----RHCGACR-LK 102
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY      109 QC---QLNSPAL 117
        :|
        :|
Db       103 RCVDIGMKKEFIL 115

RESULT 4
A:0912
vitamin D receptor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C:Accession: A60912
R:McDonnell, D.P.; Mangelsdorf, D.J.; Pike, J.W.; Haussler, M.R.; O'Malley, B.W.
Science 235, 1214-1217, 1997
A>Title: Molecular cloning of complementary DNA encoding the avian receptor for vitamin
A:Reference number: A60912; MUID:87149040; PMID:3029866
A:Accession: A60912
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 170 <MCD>
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; zinc finger

```

F;1-70/Domain: erba transforming protein homology <ERBA>

Query Match	11.48;	Score 73.5;	DB 2;	Length 70;
Best Local Similarity	35.58;	Pred. No. 1.2;		
Matches	22;	Conservative	9;	Mismatches 12;
				Indels 19;
				Gaps 5;

```
QY      50 CE-CKDWFELRABRRKEMTVSGLEKKQCPCPDHFKGVNKKTTIRHQRHNRKPNKHSBRACQDEFLK 108
        |||||:::|||    ||   |::|:|   :||: ||
Db     20 CEGCGGFFRRSMRKRAMET-----CP---FNSGCKITDNR-----RHGQACR--Lk 61
```

QY	109	QC	11
		:1	
Db	62	RC	63

## RESULT 5

C;Species: Arabidopsis thaliana (mouse-ear cress)

C/Accession: G84522	#sequence_revision 02-Feb-2001	#text_change vi-mai-2002
C/Date: 02-Feb-2001		

R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujita, C.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, C.M.; Venturi, C.M.; Sclavons, E.L.; Fraser, C.M.; Venturi, C.M.

W. J. E. & J. A. J. 1999. The biology of the plant Arabidopsis thaliana. Nature 402, 761-768.

A;Title: Sequence and analysis of chromosome 2 of the plant nucleoside transferase gene.  
A;Reference number: AB4420; MID:20083487; PMID:10617197

A/Accession: 604322  
A/Status: preliminary  
A/RefSeq: 490100.0

A; Residues: 1-108 <STO>  
A; Molecule type: UNA  
1; Cysteine reference: CB:AE002093. PTDN:AAC61287.1: GSPDB:GN00139

A;CROSS-References: BP:AB002030, MIM:300500, Locus:AB002030  
C;Genetics: 1:3000, A+2c1A900

C: Superfamily: ribherellin-regulated protein GAS2

Query Match 11.18: Score 71.5: DB

Best Local Similarity	25.98;	Pred. No. 2.7;
Matches 29;	Conservative 18;	Mismatches 38;
Indels 27;	Gaps 77;	

1 MKVLISSILL-LPLIMSMVSSSINPGVARG-----HRRGQASRRWLQEGGQCE-- 51

Db 1 MKTIVSILVLA<sup>SL</sup>LLISSLASAT<sup>IS</sup>DSAFGSGAVAPAP<sup>OS</sup>KDGPAL<sup>EC</sup>KWC--GQKCEGR 57

52 CKDWELRAPRRKENTVSGLPKKOCPDHEFGKGNVKTTRHQRHHRKPNKHSRAC 10

58 CKF---AGMKDRCLKYCGICKDCOC-----VPSGTY-----GNKHECAC 94

**RESULT 6**  
**\$35333**

steroid receptor protein svp44 - zebra fish  
C:Species: Brachydanio rerio (zebra fish)

C:\Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 24-Sep-1999  
C:\Accession: S35333

Rifjose, A.; Nornes, S.; Weber, U.; Mlodzik, M.  
EMBO J. 12, 1403-1414, 1993

A1:Title: Functional conservation of vertebrate seven-up related genes in neurogenesis  
A1:Reference number: S35333; MUID:93223680; PMID:8467797

A;Accession: S3533  
A;Molecule type: mRNA

A;Residues: 1-411 <FJ>  
A;Cross-references: EMBL:X70299; NID:g296418; PIDN:CAA9780.1; PID:g296419

C;Genetics:  
A;Gene: svp44

**C;Superfamily:** unassigned erba-related proteins; erba transforming protein homology  
**C;keywords:** DNA binding; steroid hormone receptor; zinc finger

F;74-320/Domain: erba transforming protein homology <ERBA>  
F;76-96/Region: zinc finger

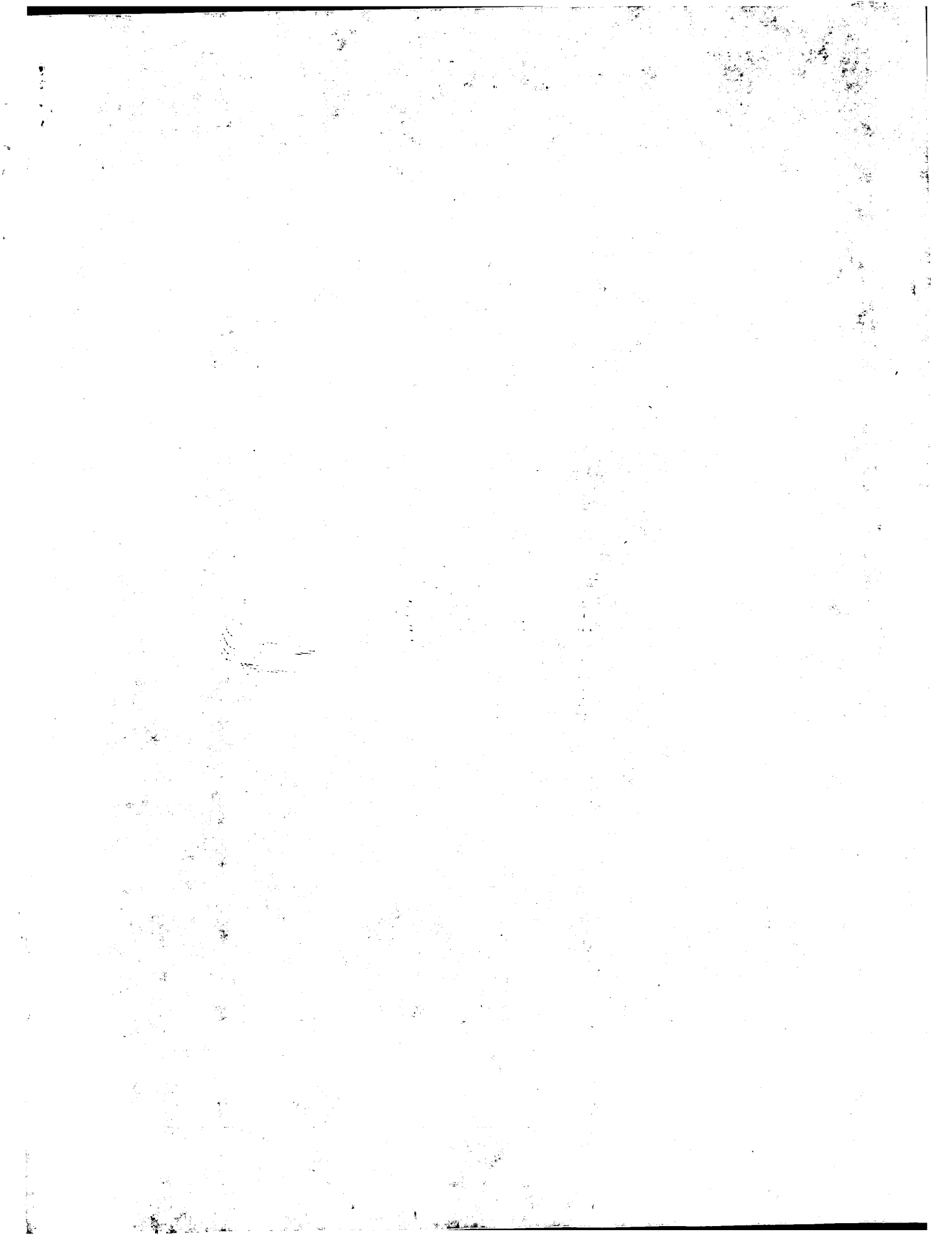
F;112-136/Region: zinc finger

```
Query match      11.0%;  score 71;  DB 2;  length 411;
```

Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987  
A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN  
A:Reference number: A28307; MUID:87317665; PMID:2819876  
A:Accession: A28307  
A:Molecule type: DNA; mRNA  
A:Residues: 1-472, 'A', 474-575 <JNC>  
A:Cross-references: GB:J02973; NID:9339658; PIDN:AAA61175.1; PID:9339659  
R:Suizuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishio, J.; Maruyama, I.; Zushi, M.; Kawah  
EMBO J. 6, 1891-1897, 1987  
A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endocyt  
A:Reference number: A29680; MUID:88004395; PMID:2820710  
A:Accession: A29680  
A:Molecule type: mRNA  
A:Residues: 1-575 <SUZ>  
A:Cross-references: GB:X05495; NID:937123; PIDN:CAA29045.1; PID:9736251  
A:Experimental source: lung endothelium  
A:Note: Part of this sequence, including the amino end of the mature protein, were deter  
R:Men, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.  
Biochemistry 26, 4350-4357, 1987  
A:Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the  
A:Reference number: A27073; MUID:88024950; PMID:2822087  
A:Accession: A27073  
A:Molecule type: mRNA  
A:Residues: 1-472, 'A', 474-575 <MEN>  
A:Cross-references: GB:M16552; NID:9339656; PIDN:AAB59508.1; PID:9339657  
A:Experimental source: placenta  
A:Note: Parts of this sequence were determined by protein sequencing  
R:Yamamoto, S.; Mitsuuchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.  
J. Biochem. 113, 433-440, 1993  
A:Title: Urinary thrombomodulin, its isolation and characterization.  
A:Reference number: JX0264; MUID:93293792; PMID:8390446  
A:Accession: JX0264  
A:Molecule type: protein; mRNA  
A:Residues: 19-472, 'A', 474-486 <YAM>  
A:Experimental source: urine  
A:Note: the urinary form appears to be identical with that circulating in plasma  
R:Gerlitz, B.; Hassell, T.; Vlahos, C.D.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.  
Biochem. J. 295, 131-140, 1993  
A:Title: Identification of the predominant glycosaminoglycan-attachment site in soluble  
serine.  
A:Reference number: S38954; MUID:94029900; PMID:8216207  
A:Accession: S38954  
A:Molecule type: protein  
A:Residues: 475-491, 'X', 493-494 <GER>  
A:Note: the residue designated 'X' was determined to be a Ser with covalently bound chon  
R:Meininger, D.P.; Komives, E.A.  
submitted to the Brookhaven Protein Data Bank, September 1995  
A:Reference number: A67363; PDB:1ZAO  
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue  
R:Tulinsky, A.; Mathews, I.I.  
A:Reference number: A52804; PDB:1HLL  
A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442  
R:Hrabal, R.; Komives, E.A.; Ni, F.  
submitted to the Brookhaven Protein Data Bank, November 1995  
A:Reference number: A65583; PDB:1FGD  
A:Contents: annotation; conformation by (1)H-NMR, residues 427-444  
R:Hrabal, R.; Komives, E.A.; Ni, F.  
Protein Sci. 5, 195-203, 1996  
A:Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the  
A:Reference number: A58595; MUID:96276211; PMID:8745396  
A:Contents: annotation; conformation by (1)H-NMR  
C:Genetics:  
A:Gene: GDB:THBD  
A:Cross-references: GDB:119613; OMIM:188040  
A:Map position: 20p11.2-20p11.2  
A:Introns: #status absent  
A:Complex: homodimer, urinary form  
C:Function:  
A:Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat  
A:Pathway: blood coagulation moderation  
A:Note: the membrane-bound form is located on the endothelium luminal surface of arterie  
A:Note: thrombin complexed with the membrane-bound form is subject to endocytosis

C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology  
C:Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood c  
e protein  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>  
F:19-513/Domain: extracellular #status predicted <EXT>  
F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>  
F:177-199/Region: C-type lectin homology <LCH>  
F:201-233/Region: EGF sequence  
F:245-280/Domain: EGF homology <EG1>  
F:288-323/Domain: EGF homology <EG2>  
F:329-362/Domain: EGF homology <EG3>  
F:369-404/Domain: EGF homology <EG4>  
F:408-439/Domain: EGF homology <EG5>  
F:445-480/Domain: EGF homology <EG6>  
F:485-513/Region: EGF sequence  
F:517-539/Domain: transmembrane #status predicted <TMN>  
F:540-575/Domain: intracellular #status predicted <INT>  
F:47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F:245-256,257-265,267-280,288-296,297-308,310-323,329-340,336-349,351-362,369-378,374  
F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
F:490,492/Binding site: chondroitin sulfate (Ser) (covalent) #status experi

Query Match 10.8%; Score 69.5; DB 1; Length 575;  
Best local similarity 23.5%; Pred. No. 19;  
Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;  
QY 5 ISSLLLLPILMSWSSSLNPGVARGHNRGASRRM---LQEGGCECKKDFLRAPR 61  
Db 209 VGSSAAVAPGLQDMCTAP--PCAVGHWAR-EPAGMDCSEVNGCEHACN----- 257  
QY 62 RRFMYVSGPKKQCP-----CHFF 80  
Db 258 ---ALPGAPRCQCPAGALQADGRSCTASATQSCNDLCERF 295  
Search completed: April 16, 2003, 12:16:36  
Job time: 20 secs



Best Local Similarity 26.3%; Pred. No. 9.7;  
Matches 26; Conservative 14; Mismatches 27; Indels 32; Gaps 6;

OY 26 PGVA--RGHRDRCQASRR-----WLAGGGECE-CKDMFLRPRKFMVSGLP 71  
DB 56 PGAGKGSQNSQSOQHIECVYCGKSSGKHVGQFTCECKSEFFKRSVRN-LTYICRA 114  
OY 72 KKQCPDHFKNVYKTRHQRHRRKPKHSRACQOFLKOC 110  
DB 115 NRMCPID-----QHRRNCOQYCR-----LKKC 136

RESULT 7  
S16664  
large protein L - parainfluenza virus type 2  
C:Species: parainfluenza virus type 2  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Jun-1999  
C:Accession: S16664  
R:Kawano, M.; Okamoto, K.; Bando, H.; Kondo, K.; Tsurudome, M.; Komada, H.; Nishio, M.;  
Nucleic Acids Res. 19, 2739-2746, 1991  
A:Title: Characterizations of the human parainfluenza type 2 virus gene encoding the L F  
A:Reference number: S16659; MUID:91252221; PMID:1645865  
A:Accession: S16664  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2262 <KAW>  
A:Cross-references: EMBL:X57559; NID:961985; PIDN:CAA40788.1; PID:961991  
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase

Query Match 11.0%; Score 71; DB 2; Length 2262;  
Best Local Similarity 26.6%; Pred. No. 43;  
Matches 29; Conservative 13; Mismatches 31; Indels 36; Gaps 6;

OY 13 PLTMSGWSLNPVGARGRDRGQAS-----RRWLQ-----EGGGECE--CK 53  
DB 421 PLILPRNAKSL-----IEQHDNALISYEYTLKMKKEISLIERKCPDPPGSELSTFMK 476

OY - 54 DWFLLRPRRKFMVSGLPKKQCPDHFKNVYKTRHQRH-RKPKHSR 101  
DB 477 DKALSPRSDMSV-----FRSLIKQRHQRHHPNPFNR 513

RESULT 8  
T13828  
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 17-Nov-2000  
R:Aikman, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G  
Nature 386, 735-738, 1997  
A:Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.  
A:Reference number: 217785; MUID:97263578; PMID:9109493  
A:Accession: T13828  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3190 <AKI>  
A:Cross-references: EMBL:088570; NID:q1916929; PID:q1916930; PIDN:AA853050.1  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0015624  
A:Map position: X  
C:Superfamily: bromodomain homology  
F:1723-1780/Domain: bromodomain homology <BRO>

Query Match 11.0%; Score 71; DB 2; Length 3190;  
Best Local Similarity 26.7%; Pred. No. 57;  
Matches 23; Conservative 11; Mismatches 30; Indels 22; Gaps 3;

OY 25 NGVARGHRDRCQASRRWLAGGGECECKDMFLRPRKFMVSGLPKKQCPDHFKNV 84  
DB 2390 NPOEA-----RKQSIORCIOSLAHQCDRANCRLP-----SCQKKKLVY 2429  
OY 85 KTRRHQRHRRKPKHSRACQOFLKOC 110

DB 2430 QHTKNCK--RKNPGCPICRQIALC 2453

RESULT 9  
T49804  
hypothetical protein B11B22.60 [Imported] - Neurospora crassa  
C:Species: Neurospora crassa  
C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T49804  
R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022  
A:Accession: T49804  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1283 <SCH>  
A:Cross-references: EMBL:AL356834; GSPDB:GNO0116; NCSP:B11B22.60  
A:Experimental source: BAC clone B11B22; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B11B22.60  
A:Map position: 6  
A:Introns: 856/2

Query Match 10.9%; Score 70.5; DB 2; Length 1283;  
Best Local Similarity 24.5%; Pred. No. 29;  
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

OY 33 RDGQASRRWLAGGGECECKDMFLRPRKFMVSGLPKKQCPDHFKNVYK--T 87  
DB 454 RKKMKKKQKKQKQKQSKGSK-----LRAPESAMPVSVWGSFSPRAMPFLPRMOGHIRGVD 508

OY 88 RHQRHNR-----RKNHSRACQOFLKOCOLRSFA 116  
DB 509 GHQSHQHMVMDGCVYRLMSEKLEPR-----QGFARLRKELALYA 550

RESULT 10  
A32693  
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 20-Sep-1999  
C:Accession: A32693  
R:Modzik, M.; Hironi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.  
Cell 60, 211-224, 1990  
A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfam  
A:Reference number: A32693; MUID:90124631; PMID:2105166  
A:Accession: A32693  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-543 <MIO>  
A:Cross-references: GB:M28863; NID:q158518; PIDN:AAA62770.1; PID:q158519  
C:Genetics:  
A:Gene: FlyBase:svp  
A:Cross-references: FlyBase:FBgn0003651  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcriptio  
F:198-452/Domain: erba transforming protein homology <ERBA>  
F:200-220/Region: zinc finger  
F:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 543;  
Best Local Similarity 26.7%; Pred. No. 16;  
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

OY 21 SSSLNCG-----VARGHRDRCQASRRWLAGGGECECKDMFLRPRKFMVSG 69  
DB 183 SQSSNSGQIDSKQNIIECVYCGKSSGKHVGQFTCEC-----CKSPFKRSVRN-LTYSC 236

OY 70 LPKQCPDHFKNVYKTRHQRHRRKPKHSRACQOFLKOC 110  
DB 237 RGSRNCPID-----QHRRNCOQYCR-----LKKC 260

